| VAX      | CRF Emors Corn  | ected by the STIC System           | 7-19 16C 432 16<br>Branch 6/14/2      |
|----------|---|------------------------------------|---------------------------------------|
| Serial N | 1 0 1/100 KUC   |                                    | CRF Processing Date:                  |
|          | Changed a file from non-ASCII to ASCI   | 1                                  | Verified by: (STIC sta                |
|          | Changed the margins in cases where the  | ne sequence text was "wrapped"     | down to the next line.                |
|          | Edited a format error in the Current App  | lication Data section, specificall | Y ENTERED                             |
|          | Edited the Current Application Data sec applicant was the prior application of      |                                    |                                       |
|          | Added the mandatory heading and subh  | neadings for "Current Application  | n Data".                              |
|          | Edited the "Number of Sequences" field  | . The applicant spelled out a nu   | umber instead of using an integer.    |
|          | Changed the spelling of a mandatory fie   | ld (the headings or subheadings    | s), specifically:                     |
|          | Corrected the SEQ ID NO when obvious  | sly incorrect. The sequence nur    | mbers that were edited were:          |
|          | Inserted or corrected a nucleic number a  | at the end of a nucleic line. SEG  | Q ID NO's edited:                     |
|          | Corrected subheading placement. All reapplicant placed a response below the s       |                                    |                                       |
|          | Inserted colons after headings/subhead  | lings. Headings edited included    | :                                     |
|          | Deleted extra, invalid, headings used by  | an applicant, specifically:        |                                       |
|          | Deleted: ☐ non-ASCII "garbage" at th ☐ page numbers throughout text; ☐              |                                    |                                       |
|          | Inserted mandatory headings, specifica  | ılly:                              |                                       |
|          | Corrected an obvious error in the response  | onse, specifically:                |                                       |
|          | Edited identifiers where upper case is u  | used but lower case is required,   | or vice versa.                        |
|          | Corrected an error in the Number of Se  | quences field, specifically:       | ·                                     |
|          | A "Hard Page Break" code was inserted   | d by the applicant. All occurrence | ces had to be deleted.                |
|          | Deleted <i>ending</i> stop codon in amino ac due to a PatentIn bug). Sequences come | •                                  | '(A)Length:" field accordingly (error |
|          | Other: replaced TYPE UK D   |                                    |                                       |
|          | poservied (A) identifier  | Jefor Cura APP DAT.                | 7                                     |

<sup>\*</sup>Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:34

INPUT SET: S32263.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
1
                                               SEQUENCE LISTING
        2
        3
                    General Information:
            (1)
                 (i) APPLICANT:
        5
-->
                       (A) NAME: Deutsches Krebsforschungszentrum Stiftung des
        7
                                  ffentlichen Rechts
                       (B) STREET: Im Neuenheimer Feld 280
        8
        9
                       (C) CITY: Heidelberg
       10
                       (E) COUNTRY: Germany
       11
                       (F) POSTAL CODE: 69120
       12
                            OF INVENTION: DNase active Protein
       13
       14
               (iii) NUMBER OF SEQUENCES: 3
       15
       16
       17
                (Av) COMPUTER-READABLE FORM:
       18
                       (A) MEDIUM TYPE: Floppy disk
       19
                       (B) COMPUTER: IBM PC compatible
       20
                       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       21
                       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
       22
       23
                      CURRENT APPLICATION DATA:
                  \rightarrow (
h) APPLICATION NUMBER: ( PCT/DE96/01016
       24
       25
           (VII) (VI) PRIOR APPLICATION DATA: NUMBER
       26
                       (A) APPLICATION DATE: DE 195 21 046.8
       27
                       (B) APPLICATION DATE: 09-JUN-1995
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       28
       29
                           FILING
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#### **ERRORED SEQUENCES FOLLOW:**

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(2) INFORMATION FOR SEQ ID NO: 1:
       31
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                  (i) SEQUENCE CHARACTERISTICS:
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                       (A) LENGTH: 2661 Base pairs
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                       (B) TYPE: Nucleotide
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                       (C) STRANDEDNESS: double
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                       (D) TOPOLOGY: linear
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                (ii) TYPE OF MOLEKULE
       39
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                     molecula TYPE:
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#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:35

INPUT SET: S32263.raw

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| 41 |  |
| 42 |  |

#### (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 795..1700

| 46       |   |      |
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| 47       | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:                          |      |
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| 49       | CTTGAACGCC TGACCTCGTA TCCACCCGCC TCAGCCTCCC AAAGTGCTGG GATTACAGGC | 60   |
| 50       |   |      |
| 51       | ATGAGCCACC ACGCCCAGCC CATAATTTAT TGATTTTTTA AAATTTGTCC AGCCTTCTAT | 120  |
| 52       |   |      |
| 53       | TACCACGTCG AATCCATTAG CTACAGCCAT CCCATGAGAA GCTGAGTGGA TTCAGCCCCA | 180  |
| 54       |   |      |
| 55       | CCTCCTGCTC ACAGACCCTG TCCGAGCACC TCATTTGTCC CAACAGCATT ACTGCAGGAC | 240  |
| 56       | COLORGIC ACAGACCOLO LOCAGACACC LOCALLIGUES CARCACCALL ACTOCAGAC   | 240  |
| 57       | CCCCAGGACG TTGGACTGCC AGCTCCCTGG GTCTCCTCCT CTCTGGGGCA GATCCTCAGT | 300  |
|          | CCCCAGGACG TTGGACTGCC AGCTCCCTGG GTCTCCTCCT CTCTGGGGCA GATCCTCAGT | 300  |
| 58       |   | 260  |
| 59       | CCTCCCTTGA CTTCACGACT GTGGCCAGAT CATGTGTGGA CTGTCCCTCT CTTTGGGTCT | 360  |
| 60       |   |      |
| 61       | CCAGAGCGCT TGCATCAAAC ACCCCTAACT CAGAAGTGTG CAGCCACACT GGGACTCAGA | 420  |
| 62       |   |      |
| 63       | ACCCAACAAC AGGGACAGAA GACTCACGCC CTTGGGGTGC CCGGTCTCGT GGCATCAGGC | 480  |
| 64       |   |      |
| 65       | ATGACTTCCA GCTCCTGCGC CTTCCCCAGC AACTGCTGAC TGGGGACCCA GACCGGGAGC | 540  |
| 66       |   |      |
| 67       | TGAGCGACGG GCCTGGCGAG CGAAGCTCGG GGTCTCACTC AGGCACCAGC CCCTCCTTGC | 600  |
| 68       |   |      |
| 69       | CCCAGGCTTG AGTGACTCAC AGCCCTATTC AGGCAGGAGC TGCTCTTCTG GGGTATCGCG | 660  |
| 70       |   |      |
| 71       | ATCCACTTAA GGATGAGGCA GACTTGGTGA CAAGCTGGTC TGAGCAGCGC TTCCAGAGCC | 720  |
| 72       |   |      |
| 73       | AGAACTGAGC CCAGTGAGAG CGCACCCTGG AGCAGCCTGG ATTCCTGGGG TGTCCCCGGC | 780  |
| 74       | AUMEDIAGE CONTINUE CONTESTED RECOCCIO                             | , 00 |
| 75       | AGCCACACAC AGCC ATG CAC TAC CCA ACT GCA CTC CTC TTC CTC ATC CTG   | 830  |
| 75<br>76 |   | 030  |
|          | Met His Tyr Pro Thr Ala Leu Leu Phe Leu Ile Leu                   |      |
| 77       | 1 5 10  |      |
| 78       |   |      |
| 79       | GCC AAT GGG GCC CAG GCC TTT CGC ATC TGC GCC TTC AAT GCC CAG CGG   | 878  |
| 80       | Ala Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala Gln Arg   |      |
| 81       | 15 20 25  |      |
| 82       |   |      |
| 83       | CTG ACA CTG GCC AAG GTG GCC AGG GAG CAG GTG ATG GAC ACC TTA GTT   | 926  |
| 84       | Leu Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr Leu Val   |      |
| 85       | 30 35 40  |      |
| 86       |   |      |
| 87       | CGG ATA CTG GCT CGC TGT GAC ATC ATG GTG CTG CAG GAG GTG GTA GAC   | 974  |
| 88       | Arg Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp   |      |
| 89       | 45 50 55 60   |      |
| 90       |   |      |
| 91       | TCT TCC GGC AGC GCC ATC CCC CTC CTG CTT CGA GAA CTC AAT CGA TTT   | 1022 |
| 92       | Ser Ser Gly Ser Ala Ile Pro Leu Leu Arg Glu Leu Asn Arg Phe       |      |
| , ,      | ber ber or, ber are the fire bed bed any ord bed ask any fire     |      |

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:35

|            |      |     |              |     |     |     |     |       |     |     |     |             |     | IN   | <b>VPUT</b> | SET: S3 | 2263.raw |
|------------|------|-----|--------------|-----|-----|-----|-----|-------|-----|-----|-----|-------------|-----|------|-------------|---------|----------|
| 93         |      |     |              |     | 65  |     |     |       |     | 70  |     |             |     |      | 75          |         |          |
| 94         |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 95         | GAT  | GGC | TCT          | GGG | CCC | TAC | AGC | ACC   | CTG | AGC | AGC | CCC         | CAG | CTG  | GGG         | CGC     | 1070     |
| 96         | Asp  | Gly | Ser          | Gly | Pro | Tyr | Ser | Thr   | Leu | Ser | Ser | Pro         | Gln | Leu  | Gly         | Arg     |          |
| 97         | -    | _   |              | 80  |     | -   |     |       | 85  |     |     |             |     | 90   | _           | =       |          |
| 98         |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 99         | AGC  | ACC | TAC          | ATG | GAG | ACG | TAT | GTG   | TAC | TTC | TAT | CGG         | TCA | CAC  | AAA         | ACA     | 1118     |
| 100        | Ser  | Thr | Tyr          | Met | Glu | Thr | Tyr | Val   | Tyr | Phe | Tyr | Arg         | Ser | His  | Lys         | Thr     |          |
| 101        |      |     | 95           |     |     |     | _   | 100   | _   |     | _   | _           | 105 |      | _           |         |          |
| 102        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 103        | CAG  | GTC | CTG          | AGT | TCC | TAC | GTG | TAC   | AAC | GAT | GAG | GAT         | GAC | GTC  | TTT         | GCC     | 1166     |
| 104        | Gln  | Val | Leu          | Ser | Ser | Tyr | Val | Tyr   | Asn | Asp | Glu | Asp         | Asp | Val  | Phe         | Ala     |          |
| 105        |      | 110 |              |     |     | _   | 115 | _     |     | _   |     | 120         | _   |      |             |         |          |
| 106        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 107        | CGG  | GAG | CCA          | TTT | GTG | GCC | CAG | TTC   | TCT | TTG | CCC | AGC         | AAT | GTC  | CTT         | CCC     | 1214     |
| 108        | Arg  | Glu | Pro          | Phe | Val | Ala | Gln | Phe   | Ser | Leu | Pro | Ser         | Asn | Val  | Leu         | Pro     |          |
| 109        | 125  |     |              |     |     | 130 |     |       |     |     | 135 |             |     |      |             | 140     |          |
| 110        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 111        | AGC  | CTG | GTG          | TTG | GTC | CCG | CTG | CAC   | ACC | ACT | CCT | AAG         | GCC | GTA  | GAG         | AAG     | 1262     |
| 112        | Ser  | Leu | Val          | Leu | Val | Pro | Leu | His   | Thr | Thr | Pro | Lys         | Ala | Val  | Glu         | Lys     |          |
| 113        |      |     |              |     | 145 |     |     |       |     | 150 |     |             |     |      | 155         |         |          |
| 114        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 115        |      |     |              |     |     | TAC |     |       |     |     |     |             |     |      |             |         | 1310     |
| 116        | Glu  | Leu | Asn          |     | Leu | Tyr | Asp | Val   |     | Leu | Glu | Val         | Ser |      | His         | Trp     |          |
| 117        |      |     |              | 160 |     |     |     |       | 165 |     |     |             |     | 170  |             |         |          |
| 118        |      |     |              |     | ~   |     |     |       |     |     |     |             |     |      |             |         |          |
| 119        |      |     |              |     |     | ATC |     |       |     |     |     |             |     |      |             |         | 1358     |
| 120        | GIN  | ser | _            | Asp | vaı | Ile | Leu |       | GTĀ | Asp | Pne | Asn         |     | Asp  | cys         | АТА     |          |
| 121        |      |     | 175          |     |     |     |     | 180   |     |     |     |             | 185 |      |             |         |          |
| 122<br>123 | ma x | ama | <b>3</b> 0 0 |     | 220 | aaa | ama | a a a | 224 | ama | ana | ama         | 000 | » cm | ana         | CON     | 1406     |
| 123        |      |     |              |     |     | CGC |     |       |     |     |     |             |     |      |             |         | 1406     |
| 125        | Ser  | 190 | 1111         | nys | гуз | Arg | 195 | изр   | цуз | ьеи | GIU | 200         | Arg | 1111 | GIU         | FIO     |          |
| 126        |      | 170 |              |     |     |     | 173 |       |     |     |     | 200         |     |      |             |         |          |
| 127        | GGC  | ጥጥር | CAC          | TGG | GTG | ATT | GCC | СΔТ   | GGG | GAG | GAC | ACC         | ACA | GTG  | CGG         | GCC     | 1454     |
| 128        |      |     |              |     |     | Ile |     |       |     |     |     |             |     |      |             |         | 1101     |
| 129        | 205  |     |              |     |     | 210 |     |       | 1   |     | 215 |             |     |      | 5           | 220     |          |
| 130        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 131        | AGC  | ACC | CAC          | TGC | ACC | TAT | GAC | CGC   | GTC | GTG | CTG | CAC         | GGG | GAG  | CGC         | TGC     | 1502     |
| 132        | Ser  | Thr | His          | Cys | Thr | Tyr | Asp | Arq   | Val | Val | Leu | His         | Gly | Glu  | Arg         | Cys     |          |
| 133        |      |     |              | -   | 225 | _   | _   | _     |     | 230 |     |             | _   |      | 235         | -       |          |
| 134        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 135        | CGG  | AGT | CTG          | CTG | CAC | ACT | GCG | GCT   | GCC | TTT | GAC | TTC         | CCC | ACG  | AGC         | TTC     | 1550     |
| 136        | Arg  | Ser | Leu          | Leu | His | Thr | Ala | Ala   | Ala | Phe | Asp | Phe         | Pro | Thr  | Ser         | Phe     |          |
| 137        |      |     |              | 240 |     |     |     |       | 245 |     |     |             |     | 250  |             |         |          |
| 138        |      |     |              |     |     |     |     |       |     |     |     |             |     |      |             |         |          |
| 139        |      |     |              |     |     | GAG |     |       |     |     |     |             |     |      |             |         | 1598     |
| 140        | Gln  | Leu |              | Glu | Glu | Glu | Ala |       | Asn | Ile | Ser | Asp         |     | Tyr  | Pro         | Val     |          |
| 141        |      |     | 255          |     |     |     |     | 260   |     |     |     |             | 265 |      |             |         |          |
| 142        |      |     |              | am  |     | ~~~ |     |       | ~~~ |     |     | <b>a-</b> - |     |      | -           |         |          |
| 143        |      |     |              |     |     | CTG |     |       |     |     |     |             |     |      |             |         | 1646     |
| 144        | GLU  |     | GLU          | ьeu | ьys | Leu |     | GIN   | АТа | HIS | ser |             | GIN | Pro  | ьeu         | ser     |          |
| 145        |      | 270 |              |     |     |     | 275 |       |     |     |     | 280         |     |      |             |         |          |

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:35

INPUT SET: S32263.raw

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| 147 | CTC ACT GTT CTG TTG CTG CTA TCA CTC CTG TCC CCT CAG CTG TGC CCT    | 1694  |  |  |  |  |
| 148 | Leu Thr Val Leu Leu Leu Ser Leu Leu Ser Pro Gln Leu Cys Pro        |       |  |  |  |  |
| 149 | 285 290 295 300  |       |  |  |  |  |
| 150 |  |       |  |  |  |  |
| 151 | GCT GCC TGAGCGTCCC CCTACCCCCC CAGGGCCTGC TGCCTTTTGG GACTTAAACC     | 1750  |  |  |  |  |
| 152 | Ala Ala  |       |  |  |  |  |
| 153 |  |       |  |  |  |  |
| 154 | t  |       |  |  |  |  |
| 155 | CCAGCCTCCC CCGTCCATCC AGCCCTGGGG CTGGGGGGCT TCAACTATAG TTGCCCTGTG  | 1810  |  |  |  |  |
| 156 |  |       |  |  |  |  |
| 157 | ACTGTAGTCC ACCCCTGCCT GCCTTGTTTG ATTTGGCTCT TGTTCTTTGG TTGGGCTTGT  | 1870  |  |  |  |  |
| 158 |  |       |  |  |  |  |
| 159 | GCCTAGATTA GGAGAGGAAG CCAGGGGCCC TGCACTCATG CCACCTGCCA GGTAGTGTAG  | 1930  |  |  |  |  |
| 160 | GCCIAGATIA GGAGAGGAG CCAGGGGCC IGCACTATI CCACCIGCA GGIAGIGIA       | 1730  |  |  |  |  |
|     | managada agaa agaa agaa agaa agaa agaa ag                          | 1000  |  |  |  |  |
| 161 | TATCAGGAGT GGAGACAAAG TGGGCTCTGG GTTGGGGTAG GGGAAGGGAG GGTTCAGAAA  | 1990  |  |  |  |  |
| 162 |  |       |  |  |  |  |
| 163 | GAGGAATGAA GATGTTGTAT GACAAGAAGG AAAGTTACTG AGAACAAAAA CCCAGATTGG  | 2050  |  |  |  |  |
| 164 |  |       |  |  |  |  |
| 165 | TGAGATAGGA CACTTGTGCA GCAGATATGC CAATGGGCCA TGTTTATTGT GGATGGGTAA  | 2110  |  |  |  |  |
| 166 | ·  |       |  |  |  |  |
| 167 | GAATCACCAG GAAACCATTA AGCCCCAATA GCTACAAGGA GGGTGGTTAA TCTGCTATAT  | 2170  |  |  |  |  |
| 168 |  |       |  |  |  |  |
| 169 | CAAACTCCTT CCCTGAAACC AGCAAACACC GGGAAACATT TTGGCTCATT ATAATCCGGT  | 2230  |  |  |  |  |
| 170 |  |       |  |  |  |  |
| 171 | GAACAATGCA GTCAGGCCTG TTATAACCGC TGAGCAGCCA CACTCGCACC TCCTGGGTGC  | 2290  |  |  |  |  |
| 172 |  | 2270  |  |  |  |  |
| 173 | TGTAGTCTGT GTTGGTACAG GCTTCTGCAT GCCTGGTAAA GTCCAGCCAA GGCTGGTCAA  | 2350  |  |  |  |  |
| 174 | TOTAGICIGI GIIGGIACAG GCIICIGCAI GCCIGGIAAA GICCAGCCAA GGCIGGICAA  | 2330  |  |  |  |  |
|     | COCARGAMON CORCAGARA ANDONOCIO ACCUMANTO COMPARARA COMPARARA CO    | 2410  |  |  |  |  |
| 175 | GGCAACATCT CCACACAGAA AATCTGCACC AGTTATGTAA GCTAAAAAGC TGTGTGAACC  | 2410  |  |  |  |  |
| 176 |  | 0.470 |  |  |  |  |
| 177 | CAGGTGTCCC GGAAAGGGGC TGCAGGACAC AGCAAAATGC CAGCAGCGTG CCGGACCCCT  | 2470  |  |  |  |  |
| 178 |  |       |  |  |  |  |
| 179 | CCCTTCCATC CTCCTCTCCA AAGAACAGAG GTCAGGAAAA ACACTGGCTG GGACGCTAGA  | 2530  |  |  |  |  |
| 180 |  |       |  |  |  |  |
| 181 | AGGGTCATGT GTTAACTATA ATCACATTTA TGGTTTGGAA CCATCACCCC AAGGTAAAAA  | 2590  |  |  |  |  |
| 182 |  |       |  |  |  |  |
| 183 | AAAAAATAAA AGGTATGTTT GGCAAAATAA AATAAAGGTA ATTAAAAAACC TAAAAAAAAA | 2650  |  |  |  |  |
| 184 |  |       |  |  |  |  |
| 185 | AAAAAAAA A   | 2661  |  |  |  |  |
| 186 |  |       |  |  |  |  |
| 187 |  |       |  |  |  |  |
|     |  |       |  |  |  |  |
| 188 | (2) INFORMATION FOR SEQ ID NO: 2:                                  |       |  |  |  |  |
| 189 | •  |       |  |  |  |  |
| 190 | (i) SEQUENCE CHARACTERISTICS:                                      |       |  |  |  |  |
| 191 | (A) LENGTH: 43 Base pairs  |       |  |  |  |  |
| 192 | (B) TYPE: Nucleotide   |       |  |  |  |  |
| 193 | (C) STRANDEDNESS: single   |       |  |  |  |  |
| 193 | (D) TOPOLOGY: linear   |       |  |  |  |  |
|     | (b) Torollogi, linear  |       |  |  |  |  |
| 195 | (ii) TYPE OF MOLECULE: other nucleic acid                          |       |  |  |  |  |
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| 197 | (A) DESCRIPTION: /desc = "DNA-Primer"                              |       |  |  |  |  |
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| PAGE: 5 |
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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:36

|   |     |   | INPUT SET: S32263.raw |
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|   | 199 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:        |                       |
|   | 200 |   |                       |
|   | 201 | CAGGGATCCG ATGACGATGA CAAAATGCAC TACCCAACTG CAC | 43                    |
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|   | 203 |   |                       |
|   | 204 | (2) INFORMATION FOR SEQ ID NO: 3:               |                       |
|   | 205 |   |                       |
|   | 206 | (i) SEQUENCE CHARACTERISTICS:                   |                       |
|   | 207 | (A) LENGTH: 27 Base pairs                       |                       |
|   | 208 | (B) TYPE: Nucleotide                            |                       |
|   | 209 | (C) STRANDEDNESS: single                        |                       |
|   | 210 | (D) TOPOLOGY: linear                            |                       |
|   | 211 |   |                       |
| > | 212 | (ii) TYPE OF MOLECULE; other nucleic acid       |                       |
| > | 213 | (A) DESCRIPTION: /desc = "DNA-Primer"           |                       |
|   | 214 |   |                       |
|   | 215 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:        |                       |
|   | 216 | ,,  |                       |
|   | 217 | GGGGGATCCT CAGGCAGCAG GGCACAG                   | 27                    |
|   | 218 |   |                       |
|   |     |   | * ·                   |

# SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:36

INPUT SET: S32263.raw

| Line | Error                           | Original Text  |
|------|---------------------------------|--|
| 5    | Mandatory Value Not Present     | (i) APPLICANT:   |
| 6    | Unknown or Misplaced Identifier | (A) NAME: Deutsches Krebsforschungszentrum Stiftung de |
| 8    | Unknown or Misplaced Identifier | (B) STREET: Im Neuenheimer Feld 280                    |
| 9    | Unknown or Misplaced Identifier | (C) CITY: Heidelberg                                   |
| 10   | Unknown or Misplaced Identifier | (E) COUNTRY: Germany                                   |
| 11   | Unknown or Misplaced Identifier | (F) POSTAL CODE: 69120                                 |
| 13   | Unknown or Misplaced Identifier | (ii) TITEL OF INVENTION: DNase active Protein          |
| 23   | Unknown or Misplaced Identifier | (v) CURRENT AAPLICATION DATA:                          |
| 27   | Unknown or Misplaced Identifier | (A) APPLICATION DATE: DE 195 21 046.8                  |
| 28   | Unknown or Misplaced Identifier | (B) APPLICATION DATE: 09-JUN-1995                      |
| 39   | Unknown or Misplaced Identifier | (ii) TYPE OF MOLEKULE: cDNA                            |
| 196  | Unknown or Misplaced Identifier | (ii) TYPE OF MOLECULE: other nucleic acid              |
| 197  | Unknown or Misplaced Identifier | (A) DESCRIPTION: /desc =                               |
| 212  | Unknown or Misplaced Identifier | (ii) TYPE OF MOLECULE: other nucleic acid              |
| 213  | Unknown or Misplaced Identifier | (A) DESCRIPTION: /desc =                               |
|      |                                 |  |

#### SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/973,815

DATE: 06/19/1999 TIME: 15:18:36

INPUT SET: S32263.raw

TITLE OF INVENTION
ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE

# **SEQUENCE CORRECTION REPORT** PATENT APPLICATION *US/08/973,815*

DATE: 06/19/1999 TIME: 15:18:36

INPUT SET: S32263.raw

Line

Original Text

Corrected Text

17

(iv) COMPUTER-READABLE FORM:

(iv) COMPUTER READABLE FORM: